Genetic Invariant Mass for Reconstruction of Resonance Decays

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Reconstruction of Resonance Decay in HEP

• Given a hypothetical RESONANCE decay topology, problems of unknown kinematic information to be reconstructed in HEP events:

  • **Combinatorial problem**
    • Many many visible objects to be tagged at correct decay vertices, which cannot be easily determined by simple kinematical cuts.

• **Missing momenta from invisible particles**
  • Neutrinos, Dark matter candidates
  • Basically resolved with kinematic constraints, given in an event / combined events.
Reconstruction of Resonance Decay in HEP

- Given a hypothetical RESONANCE decay topology, problems of unknown kinematic information to be reconstructed in HEP events:
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    - Missing momenta from invisible particles
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Momentum Reconstruction via Optimisation

- Some mass variables constructed by minimising the involved resonance mass scale:

\[ Resonances(P) \rightarrow \text{Visibles}(p) + \text{Invisibles}(q) \]

- Transverse Mass (M_T) for single resonance decay

\[ M_T^2 = \min_{q_x, q_y, q_z} (p + q)^2 \quad \text{s.t.} \quad p_T + q_T = 0 \]

- Transverse Mass (M_T2) for double resonance decays

\[ M_{T2}^2 = \min_{q_1, q_2} \left\{ \max \left[ (p_1 + q_1)^2, (p_2 + q_2)^2 \right] \right\} \quad \text{s.t.} \quad p_{1T} + p_{2T} + q_{1T} + q_{2T} = 0 \]

- Constrained-M_2/M_N with general kinematic constraints:

\[ \bar{M}^2 = \min_{q \in \mathcal{R}^n} \tilde{M}^2(p, q) \quad \text{s.t.} \quad c_i=1..m(p, q) = 0 \]
• via the optimisation (minimisation in mass scale) process, unknown momentum d.o.f are fixed by some values.

\[ \text{ex) } \text{Minimisation for } M_T \rightarrow \eta_\nu = \eta_l \]

• studied as ‘**MAOS (M_T2-Assisted On-Shell) momenta**’ for spin discrimination / mass peak reconstruction
  
  
Need New Approach for better mass variable ??

1. no more kinematic constraints (in single event)

2. scale-minimised (transverse) mass variables are unstable under the boost profile of mother resonance: Main source of systematic uncertainties in W-mass measurement

3. Its momentum solution is meaningful only for near-endpoint events.

4. While transversification, longitudinal information of visible particles are often ignored.
• Then, we try to optimise the unknown d.o.f from whole event sample collectively, in search for the solution set whose invariant distribution most likely resembles the shape of essential Breit-Wigner distribution.

• Optimisation technology = Genetic Algorithm

• Hoping to get an engineered solution/mass distribution, which evolves and approximately/ maximally inherit the boost invariant property:

=> Genetic Mass
Collective Stochastic Optimisation for Genetic Mass

<table>
<thead>
<tr>
<th>Event ID</th>
<th>1</th>
<th>2</th>
<th>...</th>
<th>N</th>
</tr>
</thead>
<tbody>
<tr>
<td>Known</td>
<td>${p_{vis}^1}$</td>
<td>${p_{vis}^2}$</td>
<td>...</td>
<td>${p_{vis}^N}$</td>
</tr>
<tr>
<td>Unknown</td>
<td>${q_{inv}^1}, C^1$</td>
<td>${q_{inv}^2}, C^2$</td>
<td>...</td>
<td>${q_{inv}^N}, C^N$</td>
</tr>
<tr>
<td>Observable</td>
<td>$f({p_{vis}^1}, {q_{inv}^1}; C^1)$</td>
<td>$f({p_{vis}^2}, {q_{inv}^2}; C^2)$</td>
<td>...</td>
<td>$f({p_{vis}^N}, {q_{inv}^N}; C^N)$</td>
</tr>
</tbody>
</table>

$\{p_{vis}^i\}$ : set of visible momenta of the event-(i)
$\{q_{inv}^i\}$ : set of unknown momenta of the event-(i)
$C^i \in \{1, ..., N_{combi}\}$ : Particle assignment ID
Dimension of the random search space:

\[ \frac{dN}{d\tilde{f}} \rightarrow \text{Physical target distribution up to the unknown model parameters} \]

\[ \tilde{f}(p, \tilde{q}; \tilde{C}) \]

Random sampling set 1

Random sampling set 2

\[ \{ (\{\tilde{q}^i\}, \tilde{C}^i) | i = 1..N_{event} \} \]

\[ N_{\text{par}} = N_{\text{event}} \times (N_q + N_{\text{combi}}) \]
Basic procedures for one random solution of the unknowns

1. Consider a random sampling of the unknowns for all event blocks.
   \[ \{ (\{ \tilde{q}^i \}, \tilde{C}^i) \mid i = 1 \ldots N_{\text{event}} \} \]

2. Select a good collider observable (non-reconstructable as \( q \) & \( C \) are unknowns):
   \[ f(p, q; C) \]

3. Calculate a sampled functional value using the sampled unknown values:
   \[ \tilde{f}(p, \tilde{q}; \tilde{C}) \]

4. Estimate the fitness as the distance between the sampled distribution and the physical target distribution where unknown model parameters are optimised to minimise distance between two distributions

\[ \text{Fitness} = \text{Distance between } \frac{dN}{df}(\tilde{\alpha}_0 = (m_0, \Gamma_0, \ldots)) \text{ and } \frac{dN}{df} \]
The Genetic Algorithm does operations, generation by generation..

1. (Initially in the 1\textsuperscript{st} generation) Consider a population of solutions (= a set of individual random solutions)

2. \textbf{Estimate the fitness} of all solutions

3. \textbf{Sort} the individuals by their ranking of the fitness

4. \textbf{Select} a portion of high ranked solutions, and discard others

5. Using \textit{reproduction} algorithm (crossover/mutation of genes) of GA, it produces children solutions, filling the missing population.

6. Estimate the fitness of new individual solutions, and sort them again by their ranking.

7. If \textbf{not converged}, goto \#5 again as the next generation.
Then, the best solution in each generation-(k), fitted into the physical target distribution which is optimized w.r.t unknown model parameters, evolves toward the true distribution,

$$\lim_{k \to \infty} \frac{dN}{df}(\tilde{\alpha}_k) = \frac{dN}{df}(\alpha_{true}) \sim \frac{dN}{df_k}$$

if the shape of our physical distribution possesses enough non-trivial physical information.

We apply this idea on the measurement of W boson mass
Reconstruction of the Breit-Wigner resonance peak of the W boson using genetic algorithm

- Unknown : Pz or rapidity of neutrino in each event
- Encoding representation for a gene : real continuous value
- Chromosome : a set of qz, \{qz\} for whole event set
- Population : randomly generated chromosomes
- Fitness (of a chromosome = a solution set) : calculated by various probability measures like chi2, log-likelihoods, relative entropy ..
- Using the (Gaussian convoluted) BW shape as a physical target distribution.
Generation = 1: Random solution
Generation = 50
Generation = 100

$\hat{M}_W$ (GeV)
Generation = 500
Generation = 2700

$M^\text{fit}_W = 79.91 \pm 0.05$ (GeV)

$\Gamma_W = 2.0$ (GeV)

$\chi^2/\text{ndf} = 1.11$
Conclusions

• We are engineering to produce the Genetic Mass which resembles the properties of BW resonance.

• Genetic Algorithm, based on the principle of Natural Selection, is found to be very efficient and powerful for implementing the collective stochastic optimisation.

• Collective stochastic optimisations in light of stable physical target distribution can provide a good chance to solve complicated event reconstruction problems
Backup
Genetic Algorithm

• Genetic algorithm is a search and optimisation technique based on Darwin’s Principle of Natural Selection.

• “Select the best individuals with good fitness, and Exchange good genes, and Select ..”

• Optimises a large number of (continuous/discrete) parameters with extremely complex objective function. It can rather easily jump out of a local minimum, in compared to the usual gradient-based search algorithms.

• Does not require derivative information.

• May encode the parameters so that the optimisation is done with the encoded parameters.
Simple GA works with the binary encoding for each variable.

\[
gene^i = \text{an encoded unknown value (} q^i \text{ or } C^i \text{) of an event block}
\]

\[
\text{chromosome} = \begin{pmatrix}
Gene^1 & Gene^2 & \ldots & Gene^{N_{\text{event}}}
\end{pmatrix}
\]

\[
(= \text{individual}) = \text{a set of genes = a set of encoded unknowns} \\
\leftrightarrow \{ \tilde{q}^1 / \tilde{\bar{C}}^1, \tilde{q}^2 / \tilde{\bar{C}}^2, \ldots, \tilde{q}^{N_{\text{event}}} / \tilde{\bar{C}}^{N_{\text{event}}} \}
\]

\[
\rightarrow \text{A distribution of } \{ \tilde{m}(p^i, \tilde{q}^i | \tilde{\bar{C}}^i) \}
\]

\[
\text{population} = \text{set of (random)chromosomes} \\
\leftrightarrow \text{set of (random)solutions} \\
\rightarrow \text{larger population} \rightarrow \text{better genetic diversity} \\
\rightarrow \text{GA can survey larger solution space.}
\]

\[
\text{fitness} = \text{quality of a solution}
\]
Flow-chart of Genetic Algorithm

1. Encode Chromosomes
   1.1 Binary encoding
   1.2 Continuous encoding

2. Generating initial population

3. Evaluation of fitness values of all chromosomes

4. Convergence test (continue, if not converged)

5. Selection and Mating
   5.1 Roulette Wheel Selection in proportion to fitness

6. Reproduction (Crossover, Mutation)
From ‘Practical Genetic Algorithms’ by Haupt.
Reproduction operators

- Crossover: random points are chosen on the individual chromosomes and the genes are exchanged at this point. This is the first operation where the GA explores another points in the variable space.
e.g. ) single point crossover

\[
\begin{align*}
1010101 & | 0001 \\
0101010 & | 1110 \\
\rightarrow 1010101 & | 1110 \\
0101010 & | 0001
\end{align*}
\]
- Mutation: this is the process by which a bit/string is deliberately changed so as to maintain diversity in the population set

\[
\text{\# of mutations} = \mu \times (N_{\text{pop}} - N_{\text{elite}}) \times N_{\text{bits}},
\]

\[
\mu = \text{mutation rate}
\]
- Clustering of the showered remnants by their partonic origins

• Easy example

1. Clustering 4 particles into two groups by their (resonant) decay origins

2. Clustering N-particles into M-groups by their origins
1. Grouping 4 visible momenta into 2 pairs - \((a_1,b_1), (a_2,b_2)\) by their origins - 2 on-shell mother particles, each decays to \((a_i, b_i)\), without the knowledge of \(M_{\text{mother}}\).

\((N_{\text{event}} = 100, N_{\text{pop}} = 1000, \text{Elite rate} = 0.2, \mu = 0.25)\)

(Fitness = Height of the peak)

1st generation:
Best chromosome: 0001110.......2112020
fitness: 98, Nfalse: 51, NEvent: 100

....

42nd generation:
Best chromosome: 0000..1..00000000000
fitness: 198, Nfalse: 1, NEvent: 100
Running time - Real Time : 3.846, Cpu : 3.610 s
Gain:

1. Naive search: \# of fitness estimation \sim 3^{100} = 59049^{10} → may not be possible before the end of the universe.

2. Stochastic search using GA: \# of fitness estimation \sim \frac{N_{pop}}{2} \times N_{gen} = 500 \times 42 = 21000 !!! → just 3-sec using an old single core.
Precise W mass measurement - Motivation

• In the Electroweak theory of the SM, W mass is predictable

\[ M_W = \sqrt{\frac{\pi \alpha}{\sqrt{2} G_F \sin \theta_W}} \frac{1}{\sqrt{1 - \Delta r}} \]

One loop radiative correction \( \Delta r \) to W mass depends quadratically on the top mass, and logarithmically on Higgs mass.

Measuring \( M_w \) and \( M_t \), one can extract the information on \( M_H \), vice versa.

Some new physics can contribute on the \( M_w \)
With the discovery of the Higgs and direct Higgs mass measurement..

- Global EW fitting with MH(exp) indirectly estimated MW and $\Delta MW \sim 8$ MeV
- Compared to the $\Delta Mt(exp) \sim 0.9$ GeV, precision on $\Delta MW(exp) \sim 5$ MeV is required assuming equivalent contribution on Higgs mass precision.
- Both values motivate some improvements on current experimental precision, $\Delta MW \sim 15$ MeV → Precision MW measurement is one of the key EW precision tests for the SM consistency.
Precision W mass measurement - Status

- World average: \(80385 \pm 15\) MeV (sys+stat)

- CDF result (80375 MeV, 2012)
  - D0 (80387 MeV 2012)

- Systematic uncertainty, (CDF:15, D0: 22) MeV > Statistical uncertainty, (CDF:22, D0: 13) MeV

- How to reduce the systematic uncertainties?
Systematic uncertainties on MW measurement

1) Experimental sources

1) Lepton energy scale/energy resolution/shower model/energy loss/efficiencies

2) Backgrounds

3) Recoil model
   : limited by the size of the Z->ll sample => Enhanced event statistics can help.

2) W and Z production and decay models

1) PDF : Boost of W-boson along longitudinal beam direction does not change a MT value. However uncertainty on the PDF affects on event acceptance rate, in particular with respect to the imposed pseudo-rapidity range, so MT distribution is also changed.

2) Transverse momentum of W boson : PT(l) distribution is very sensitive on the non-zero PT(W). MT distribution is also affected by W boson’s PT.

3) Photon radiation (QED) : final state radiation from lepton
Measurement strategy and sources of systematic uncertainty

- W-boson production and decay

- Template method, using MT, PT(lepton) and PT(neutrino) variables

\[ M_T = \sqrt{2P_T^l P_T^{\nu}(1 - \cos(\phi^l - \phi^{\nu}))} \]

- The distributions of the variables are unstable w.r.t the momentum profile of the mother particle, W production

  - Both MT and PT(l) distributions are not invariant under PT(W) and PDF.
  - One solution is to do precise calculation and simulation on the W production (and decay) to reduce the systematic uncertainties literally.
Consider a ‘sampled invariant mass’ of $W$, where the missing momentum along beam direction is assigned by random variable

$$\tilde{M}_W(p^l, p_T^\nu; \tilde{p}_z^\nu)^2 \equiv \left( p^l + \tilde{p}^\nu \right)^2 \quad \text{with} \quad \tilde{p}^\nu = (\sqrt{P_T^\nu + \tilde{p}_z^\nu^2}, p_x^\nu, p_y^\nu, \tilde{p}_z^\nu),$$

$$= 2 \left[ |p^l| \sqrt{p_T^\nu + \tilde{p}_z^\nu^2} - P_T^\nu \cdot p_T^\nu - p_z^l \tilde{p}_z^\nu \right],$$

$$= 2 |p_T^l| |p_T^\nu| \left[ \cosh(\eta^l - \tilde{\eta}^\nu) - \cos \phi_{l\nu} \right],$$

In this picture, $M_T$ is also one sampled invariant mass of $W$, but which is especially optimised to minimise the mass scale.

$$M_T(W) \equiv \min_{\tilde{p}_z} \tilde{M}_W \quad \rightarrow \quad \tilde{\eta}^\nu = \eta^l$$